



## SEQUENCE LISTING

<110> Rauch, Charles  
Walczak, Henning

<120> RECEPTOR THAT BINDS TRAIL

<130> 2625-E

<140> US 09/378,045

<141> 1999-08-20

<150> US 08/883,036

<151> 1997-06-26

<150> US 08/869,852

<151> 1997-06-04

<150> US 08/829,536

<151> 1997-03-28

<150> US 08/815,255

<151> 1997-03-12

<150> US 08/799,861

<151> 1997-02-13

<160> 5

<170> PatentIn version 3.0/ Microsoft Word, Version 6.0.1

<210> 1

<211> 1323

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1323)

<400> 1

atg gaa caa cgg gga cag aac gcc cgg gcc gct tcg ggg gcc cgg aaa 48  
Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys  
1 5 10 15

agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ccc 96  
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro  
20 25 30

cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg 144  
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu  
35 40 45

gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag	192
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln	
50 55 60	
cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg	240
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu	
65 70 75 80	
tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc	288
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser	
85 90 95	
tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc	336
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe	
100 105 110	
tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccg	384
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro	
115 120 125	
tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc	432
Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe	
130 135 140	
cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt	480
Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys	
145 150 155 160	
ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc	528
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile	
165 170 175	
gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca	576
Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro	
180 185 190	
gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc	624
Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro	
195 200 205	
tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc	672
Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val	
210 215 220	
ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc	720
Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val	
225 230 235 240	
ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag	768
Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu	
245 250 255	
cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc	816
Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu	
260 265 270	
aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa	864
Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu	
275 280 285	

Sub  
B.1  
Cont

atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac atg ttg tcc	912
Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser	
290 295 300	
ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct gaa agg tct	960
Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser	
305 310 315 320	
cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat ccc act gag	1008
Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu	
325 330 335	
act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc ttt gac	1056
Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp	
340 345 350	
tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat gag ata	1104
Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile	
355 360 365	
aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg tac acg	1152
Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr	
370 375 380	
atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct gtc cac	1200
Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His	
385 390 395 400	
acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc aag cag	1248
Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln	
405 410 415	
aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat cta gaa	1296
Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu	
420 425 430	
ggt aat gca gac tct gcc atg tcc taa	1323
Gly Asn Ala Asp Ser Ala Met Ser	
435 440	

<210> 2  
 <211> 440  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys	
1 5 10 15	
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro	
20 25 30	
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu	
35 40 45	
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln	
50 55 60	

Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
 65 70 75 80  
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser  
 85 90 95  
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe  
 100 105 110  
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro  
 115 120 125  
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe  
 130 135 140  
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys  
 145 150 155 160  
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile  
 165 170 175  
 Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro  
 180 185 190  
 Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro  
 195 200 205  
 Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val  
 210 215 220  
 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val  
 225 230 235 240  
 Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu  
 245 250 255  
 Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu  
 260 265 270  
 Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu  
 275 280 285  
 Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser  
 290 295 300  
 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser  
 305 310 315 320  
 Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu  
 325 330 335  
 Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp  
 340 345 350  
 Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile  
 355 360 365  
 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr  
 370 375 380

Sub  
 B1  
 cont

Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His  
385 390 395 400

Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln  
405 410 415

Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu  
420 425 430

Gly Asn Ala Asp Ser Ala Met Ser  
435 440

<210> 3  
<211> 157  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (3)..(155)

<220>  
<221> Unsure  
<222> (145)..(145)  
<223> n = a, t, g, c

<220>  
<221> Unsure  
<222> (149)..(149)  
<223> n = a, t, g, c

<400> 3  
ct gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc 47  
Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro  
1 5 10 15

ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat 95  
Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn  
20 25 30

gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg 143  
Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu  
35 40 45

tnc acn atg ctg at 157  
Xaa Thr Met Leu  
50

<210> 4  
<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 4

Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe  
1 5 10 15

Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu  
20 25 30

Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa  
35 40 45

Thr Met Leu  
50

<210> 5  
<211> 8  
<212> PRT  
<213> Artificial

<220>  
<223> FLAG peptide  
<400> 5

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5